In the Specification:

Replace the paragraph beginning at page 19, line 27, with the following rewritten paragraph:

Ds mobility is achieved by crossing the Ds-containing plants (DsG, DsE and Ds378-GUS) with a transposase-producing plant transformed with Bam35S-Ac. In this construct, Ac transposase is produced under the control of the 35S promoter fused to an Ac element whose 5' terminal region, up to the unique BamHI site has been deleted. Chlorosulfuron resistance (Chl^r) is obtained upon excision of the Ds element from the Ds378-GUS-containing construct and activation of a mutated acetolactate synthase gene from GUS-containing construct and activation of a mutated acetolactate synthase gene from *Arabidopsis* (Fedoroff and Smith, 1993). Excision footprints (Ex1 and Ex2 SEQ ID NO's:3 and 4 respectively) were obtained upon excision of Ds378-GUS in the F1 of crosses between Bam35S-Ac and Ds378-GUS and amplified with primers pr1 (SEQ ID NO:2) and pr2 (SEQ ID NO:1). The sequence flanking Ds378-GUS is shown above Ex1 and Ex2. The underlined sequence indicates the host duplication flanking Ac insertion site in the original *wx-m7* maize allele from which Ds378-GUS was derived.

Replace the paragraph beginning at page 20, line 32, with the following rewritten paragraph:

(4) DNA analysis. DNA was extracted from young leaves by the Dellaporta method (Dellaporta et al., 1983), with an additional phenol chloroform extraction. PCR reactions were performed using Promega *Taq* polymerase according to conditions recommended by the manufacturers, with 2.5 mM $MgCl_2$, and 200 μM dNTPs in an MJ thermocycler. The following program was used: 2 min denaturation at 94°C and 30 cycles of 1 min at 94°C, 45 min at 55°C, 1 min at 72°C, and a final step of 5 min at 72°C. The primers used to amplify *Ds* excision products were: pr2, 5' GGATAGTGGGATTGTGCGTC 3' (SEQ ID NO:1), which is complementary to sequences in the 35S promoter, and prl, 5' GGATGATTTGTTGGGGTTTA 3' (SEQ ID NO:2), which is complementary to sequences in the ALS gene (Figure 3). Bands of the expected size for excision products (ca. 322 bp) were extracted from the agarose gel, and DNA was purified using GenClean according to the manufacturer's

instructions. These PCR products were cloned into a pGEM-T vector (Promega) and sequenced using the T7 or SP6 primers. For Southern analysis, 2 of μg genomic DNA was digested with *Hind*III, fractionated on 0.8% agarose gels, and transferred to a nitrocellulose membrane purchased from MSI. Hybridization was performed according to manufacturer's instructions. An internal GUS fragment of 1 kb was amplified by PCR, radiolabeled by the random priming method (Feinberg and Vogelstein, 1983), and used as a probe for *Ds* detection.

After Page 35, please add the attached Sequence Listing.